

AMENDMENTS TO THE CLAIMS:

Claims 1-32 are canceled without prejudice or disclaimer. Claims 33-64 are added. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-32 (Cancelled.)

33. (New.) A variant of a parent fungal cutinase, wherein the parent cutinase is at least 70% homologous to SEQ ID NO:1, wherein the variant has above 80% homology to its parent and comprises a modification of at least one amino acid residue corresponding to position A4, T29, A88, N91, A130, Q139, I169, I178 or R189 in SEQ ID NO:1; and wherein the variant has cutinase activity.

34. (New.) The variant claim 33, which comprises the substitution A4V, T29M/I/C, A88H/L/V, N91H, A130V, Q139R, I169A/G/T/V, I178V or R189A/H/V.

35. (New.) The variant of claim 33, wherein the parent cutinase is the cutinase from *H. insolens* strain DSM 1800.

36. (New.) The variant of claim 33, wherein the parent cutinase is at least 80% homologous to SEQ ID NO:1.

37. (New.) The variant of claim 33, wherein the variant cutinase has above 85% homology to its parent.

38. (New.) The variant of claim 33, wherein the variant cutinase has above 90% homology to its parent.

39. (New.) The variant of claim 33, wherein the variant cutinase has above 95% homology to its parent.

40. (New.) The variant of claim 33, which further comprises at least one amino acid substitution at a position corresponding to Q1, L2, E6, G8, E10, S11, A14, N15, A16, F24, V38, N44, L46, E47, S48, H49, R51, D63, L66, S116, S119, G120, L138, T164, T166, L167, I168, L174 and/or E179, using of SEQ ID NO:1 for numbering.

41. (New.) The variant of claim 33, which variant further comprises at least one amino acid substitution at a position corresponding to Q1P/C/L, L2K/Q/V, E6Q, G8D, E10Q, S11C/T, A14P, N15T/D, A16T, F24Y, V38H, N44D, L46I, E47K, S48/E/K, H49Y, R51P, D63N, L66I, S116K, S119P, G120D, L138I, T164S, T166M/I, L167P, I168F, L174F and/or E179Q, using SEQ ID NO:1 for numbering.

42. (New.) The variant of claim 33, which variant further comprises substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q, using SEQ ID NO:1 for numbering.

43. (New.) The variant of claim 33, which variant has hydrolytic activity towards terephthalic acid esters.

44. (New.) The variant of claim 33, which variant has hydrolytic activity towards cyclic tri(ethylene terephthalate) and/or Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate.

B3
conf
45. (New.) The variant of claim 33, which has a denaturation temperature which is at least 5° higher than the parent cutinase at pH 8.5.

46. (New.) The variant of claim 33, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q, using SEQ ID NO:1 for numbering.

47. (New.) The variant of claim 33, wherein the patent cutinase has the amino acid sequence of SEQ ID NO:1 and wherein the variant comprises the substitutions corresponding to E6Q +A14P +E47K +R51P +A130+E179Q.

48. (New.) The variant of claim 33, wherein the patent cutinase has the amino acid sequence of SEQ ID NO:1 and the variant comprises the substitutions corresponding to E6Q+ A14P +N15D +E47K +R51P +A130+E179Q.

49. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A4.

50. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to T29.

51. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A88.

52. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to N91.

53. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A130.

54. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to Q139.

55. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to I169.

56. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to I178.

57. (New.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to R189.

58. (New.) A variant of a parent fungal cutinase, wherein the parent cutinase is at least 70% homologous to SEQ ID NO:1, wherein the variant differs from the parent cutinase by 1 to 20 substitutions; and wherein said substitutions comprise a modification of at least one amino acid residue corresponding to position A4, T29, A88, N91, A130, Q139, I169, I178 or R189 in SEQ ID NO:1; and wherein the variant has cutinase activity.

59. (New.) A variant of a parent cutinase, wherein the parent cutinase is at least 70% homologous to SEQ ID NO:1, and wherein the variant has above 80% homology to its parent and comprises a substitution selected from the following group of substitutions using SEQ ID

NO:1 for numbering:

S48E +A88H +N91H +R189V;

Q1L +L2K +G8D +N15D;

N44D +A130V;

Q1C +L2V +G120D;

A88L +R189A;

S48E +L66I +A88L +I169A +R189H;

A88V +S116K +S119P +Q139R +I169V +R189V;

A88V +R189A;

S48K +A88H +I169G +R189H;

Q1L +L2Q +A4V +S11T;

T164S;

L174F;

H49Y;

Q1L +L2K +G8D +N15D +S48E +A88H +N91H +R189V;

Q1L +L2K +G8D +N15D +N44D +A130V;

Q1L +L2K +G8D +N15D +S48E +A88H +N91H +A130V +R189V;

G8D +N15D +A16T;

A130V;

Q1C +L2V;

G8D +N15D +A16T;

G8D +N15D +S48E +A88H +N91H +A130V +R189V;

G8D +N15D +T29M +S48E +A88H +N91H +A130V +R189V;

G8D +N15D +T29I +S48E +A88H +N91H +A130V +R189V;

G8D +N15D +T29C +S48E +A88H +N91H +A130V +R189V;

G8D +N15D +S48E +A88H +N91H +A130V +L174F +I178V +R189V;

G8D +N15D +S48E +A88H +N91H +A130V +T166M +I168F +R189V;

G8D +N15D +S48E +A88H +N91H +A130V +T166I +L167P +R189V;

G8D +N15D +V38H +S48E +A88H +N91H +A130V +I169T +R189V;

G8D +N15D +V38H +S48E +A88H +N91H +A130V +R189V; and

G8D +N15D +T29M +S48E +A88H +N91H +A130V +T166I +L167P +R189V;

and wherein the variant has cutinase activity.

60. (New.) The variant of claim 59, wherein the parent cutinase is the cutinase from *H. insolens* strain DSM 1800.

61. (New.) The variant of claim 59, wherein the parent cutinase is at least 80% homologous to SEQ ID NO:1.

62. (New.) The variant of claim 59, wherein the variant cutinase has above 85% homology to its parent.

63. (New.) The variant of claim 59, wherein the variant cutinase has above 90% homology to its parent.

64. (New.) The variant of claim 59, wherein the variant cutinase has above 95% homology to its parent.

65. (New.) The variant of claim 59, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q, using SEQ ID NO:1 for numbering.